



<110> ARKHAMMAX Per 00. et al.

<120> AN IMPROVED METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE

<130>	0459	-0571	lΡ												
<140> <141>	09/80 2001														
<160>	40														
<170>	Pate	ntIn	vers	sion	3.1										
<210> <211> <212> <213>	1 1788 DNA Aeque	orea	vict	coria	a and	d moi	ıse								
<220> <221> <222> <223>	CDS (1).	. (178	38)												
<400> atg gg Met Gl															48
aaa ga Lys Gl															96
gac cc Asp Pr															144
acc ct Thr Le 50															192
gag ag Glu Se 65	r Gly		His	Tyr	Ala	Met	Lys	Ile	Leu	Asp	Lys	Gln	Lys	Val	240
gtg aa Val Ly															288
cag gc															336

					tac Tyr									384
_					cgg Arg						-	-		432
					cag Gln 150									480
					cgg Arg									528
					cag Gln									576
					acc Thr									624
			_	-	aaa Lys				_	-		_	 	672
		-			tac Tyr 230		_	-	-					720
_	_	-			cag Gln						_			768
					ttc Phe	_		-	_	_	_	_		816
					cta Leu									864
					aac Asn									912
					aag Lys 310									960
					agt Ser									1008

					gag Glu										1056
					gga Gly										1104
					ggc Gly										1152
			-		gat Asp 390	-									1200
			Thr		aag Lys										1248
					gtt Val		-								1296
					ttc Phe										1344
_	_				tac Tyr		-	_				_	_	-	1392
-	-	_		-	ggt Gly 470	-									1440
		-			gaa Glu	_							_	-	1488
					cat His		-			_	•	_		_	1536
				-	aac Asn				_				_		1584
_	-			-	gac Asp									-	1632
		-			cca Pro 550	-									1680

	tcc Ser															17	28
	gta Val															17	76
	cag Gln		taa													17	88
	1> 5	2 595 PRT Aequo	orea	vict	coria	a and	d moi	ıse									
<40	0> 2	2															
Met 1	Gly	Asn	Ala	Ala 5	Ala	Ala	Lys	Lys	Gly 10	Ser	Glu	Gln	Glu	Ser 15	Val		
Lys	Glu	Phe	Leu 20	Ala	Lys	Ala	Lys	Glu 25	Asp	Phe	Leu	Lys	Lys 30	Trp	Glu		
Asp	Pro	Ser 35	Gln	Asn	Thr	Ala	Gln 40	Leu	Asp	Gln	Phe	Asp 45	Arg	Ile	Lys		
Thr	Leu 50	Gly	Thr	Gly	Ser	Phe 55	Gly	Arg	Val	Met	Leu 60	Val	Lys	His	Lys		
Glu 65	Ser	Gly	Asn	His	Tyr 70	Ala	Met	Lys	Ile	Leu 75	Asp	Lys	Gln	Lys	Val 80		
Va]	Lys	Leu	Lys	Gln 85	Ile	Glu	His	Thr	Leu 90	Asn	Glu	Lys	Arg	Ile 95	Leu		
Glr	Ala	Val	Asn 100	Phe	Pro	Phe	Leu	Val 105	Lys	Leu	Glu	Phe	Ser 110	Phe	Lys		
Asp	Asn	Ser 115	Asn	Leu	Tyr	Met	Val 120	Met	Glu	Tyr	Val	Ala 125	Gly	Gly	Glu		
Met	Phe 130	Ser	His	Leu	Arg	Arg 135	Ile	Gly	Arg	Phe	Ser 140	Glu	Pro	His	Ala		

Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser 145 150 155 160

Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp 165 170 175

Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val 180 185 190

Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro
195 200 205

Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala 210 215 220

Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe 225 230 235 240

Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val 245 250 255

Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn 260 265 270

Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly 275 280 285

Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile 290 295 300

Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys 305 310 315 320

Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile 325 330 335

Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly 340 345 350

Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 355 360 365

Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser 370 375 380

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe 385 390 395 400

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr 405 410 415

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met 420 425 430

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln 435 440 445

Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala 450 455 460

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 465 470 475 480

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu 485 490 495

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys 500 505 510

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly 515 520 525

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 530 540

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala 545 550 555 560

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu 565 570 575

Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 580 585 590

Pro Gln Glu 595			
<210> 3 <211> 2751 <212> DNA <213> Aequorea vio	ctoria and mouse		
<220> <221> CDS <222> (1)(2751) <223>	•		
		tcc acg gcg tct cag Ser Thr Ala Ser Gln 10	
		ctg agg cag aag aac Leu Arg Gln Lys Asn 30	
		cgc ttc ttc aag caa Arg Phe Phe Lys Gln 45	
		tgg ggg ttt ggg aaa Trp Gly Phe Gly Lys 60	
		gtt cat aag agg tgc Val His Lys Arg Cys 75	
		gat aag gga cct gac Asp Lys Gly Pro Asp 90	
		atc cac aca tac gga Ile His Thr Tyr Gly 110	
		ctc tat gga ctt atc Leu Tyr Gly Leu Ile 125	
		aat gtt cac aac cag Asn Val His Asn Gln 140	
		gat cac aca gag aag Asp His Thr Glu Lys 155	

			gct Ala									528
			aat Asn									576
			ctg Leu									624
-			acc Thr		-		-					672
			aaa Lys 230									720
			gac Asp									768
			ggt Gly	-			-	_		-		816
 		_	cac His									864
			gat Asp									912
	_	_	cta Leu 310			_			_		_	960
			caa Gln									1008
			ctc Leu									1056
			agg Arg									1104
			gtg Val									1152

					gtg Val 390										1200
					tgc Cys										1248
					ggc Gly										1296
			-		cca Pro		-	-			-	-			1344
					ctt Leu										1392
_				_	atg Met 470				_	,,,				_	1440
					aag Lys										1488
		_			ccg Pro	_			-				-		1536
_	_			_	tct Ser										1584
		_		-	ggg Gly	_									1632
-	_		-		ata Ile 550	_									1680
_		_	-	-	gtc Val			-							1728
	_	_	_	_	ggc Gly	_									1776
_		_			agg Arg										1824

						_				_			gga Gly	-	-	1872
		_	_				_		-		-		aca Thr			1920
													gaa Glu			1968
_		_			_						_		agt Ser 670	-	-	2016
													gtt Val			2064
		_	-		-		_	-					ttc Phe		-	2112
													acc Thr			2160
													acg Thr			2208
						_		-			_		cca Pro 750	_		2256
_		_		_			_	_	_	_		_	ggt Gly		_	2304
_	_	_						-	-				aag Lys		_	2352
-	_	_	_		-		-			-		_	atc Ile			2400
			_			-	-						cac His		-	2448
								-			_	-	gac Asp 830			2496

Lys Asn Gly Ile Lys Val 835		t aga cac aac att e Arg His Asn Ile 845	
gga agc gtt caa tta gca Gly Ser Val Gln Leu Ala 850	_		
gat ggc cct gtc ctt tta Asp Gly Pro Val Leu Leu 865 870			
gcc ctt tcc aaa gat ccc Ala Leu Ser Lys Asp Pro 885		g Asp His Met Ile	
gag ttt gta aca gct gct Glu Phe Val Thr Ala Ala 900			
aaa cct cag gag taa Lys Pro Gln Glu 915			2751
<210> 4 <211> 916			
<212> PRT <213> Aequorea victoria	a and mouse		
	a and mouse		
<213> Aequorea victoria		r Thr Ala Ser Gln	Asp Val
<213> Aequorea victoria <400> 4 Met Ala Asp Val Tyr Pro	Ala Asn Asp Se:		15
<213> Aequorea victoria <400> 4 Met Ala Asp Val Tyr Pro 1 5 Ala Asn Arg Phe Ala Arg	Ala Asn Asp Se: 10 Lys Gly Ala Let 25	u Arg Gln Lys Asn 30	Val His
<213> Aequorea victoria <400> 4 Met Ala Asp Val Tyr Pro 1 5 Ala Asn Arg Phe Ala Arg 20 Glu Val Lys Asp His Lys	Ala Asn Asp Se: 10 Lys Gly Ala Lei 25 Phe Ile Ala Ard 40	u Arg Gln Lys Asn 30 g Phe Phe Lys Gln 45	Val His Pro Thr
<pre><213> Aequorea victoria <400> 4 Met Ala Asp Val Tyr Pro 1</pre>	Ala Asn Asp Ser 10 Lys Gly Ala Ler 25 Phe Ile Ala Ard 40 Asp Phe Ile Try 55	u Arg Gln Lys Asn 30 g Phe Phe Lys Gln 45 p Gly Phe Gly Lys 60	Val His Pro Thr Gln Gly

Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro 100 105 110

Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln 115 120 125

Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val 130 135 140

Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly 145 150 155 160

Arg Ile Tyr Leu Lys Ala Glu Val Thr Asp Glu Lys Leu His Val Thr
165 170 175

Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser 180 185 190

Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser 195 200 205

Lys Gln Lys Thr Lys Thr Ile Arg Ser Asn Leu Asn Pro Gln Trp Asn 210 215 220

Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu 225 230 235 240

Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met 245 250 255

Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser 260 265 270

Gly Trp Tyr Lys Ala His Asn Gln Glu Glu Glu Glu Tyr Tyr Asn Val 275 280 285

Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys 290 295 300

Phe Glu Lys Ala Lys Leu Gly Pro Val Gly Asn Lys Val Ile Ser Pro 305 310 315 320

Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu 325 330 335

Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys 340 345 350

Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys 355 360 365

Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Val Glu Cys Thr 370 375 380

Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu 385 390 395 400

Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val 405 410 415

Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val 420 425 430

Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser $435 \hspace{1.5cm} 440 \hspace{1.5cm} 445$

Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu 450 460

Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala 465 470 475 480

Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg 485 490 495

Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr 500 505 510

Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu 515 520 525

Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp 530 540

Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser 550 545 Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln 570 565 Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg 585 Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg 600 Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu 615 Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro 630 635 Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe 650 645 Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val 665 670 Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 675 680 685 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val 695 690 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 710 715 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val 725 730

Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His 740 745 750

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 755 760 765 Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg 775 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 795 785 790 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met 810 805 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp 840 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly 855 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser 865 870 875 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu 885 890 Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr 905 Lys Pro Gln Glu 915 <210> 5 <211> 1896 <212> . DNA <213> Aequorea victoria and human <220> <221> CDS <222> (1)..(1896) <223> <400> 5 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 5 10

					gac Asp											96
					gcc Ala											144
					ctg Leu											192
_					cag Gln 70	_		_	_							240
					aag Lys											288
_					aag Lys	_	_				_		_	_		336
	_				gac Asp		_			_			_			384
					gac Asp											432
			_		aac Asn 150	-			_	-	-					480
		_			ttc Phe	_										528
	_		_	_	cac His		_	_						_		576
		_	_		gac Asp					-		-		-	_	·624
-		-			gag Glu											672
		_	-		atc Ile 230											720

		_		_	-	caa Gln	_	_				_			 768
						ggc Gly									816
	_		-	-		gag Glu			_		_		_	_	864
						acg Thr 295									912
						gcc Ala									960
						ccc Pro									1008
						atc Ile									1056
						ctg Leu		Ala							1104
						gac Asp 375									1152
						agc Ser									1200
_		_				aag Lys									1248
_	_		-			aac Asn	_		-				_	_	1296
-		_	-			ctg Leu	_			-	_				1344
						gag Glu 455									1392

cca gag atc atg ctg aac tcc aag ggc tat acc aag tcc atc gac atc Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile 465 470 475 480	1440
tgg tct gtg ggc tgc att ctg gct gag atg ctc tct aac cgg ccc atc Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile 485 490 495	1488
ttc cct ggc aag cac tac ctg gat cag ctc aac cac att ctg ggc atc Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile 500 505 510	1536
ctg ggc tcc cca tcc cag gag gac ctg aat tgt atc atc aac atg aag Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys 515 520 525	1584
gcc cga aac tac cta cag tct ctg ccc tcc aag acc aag gtg gct tgg Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp 530 535 540	1632
gcc aag ctt ttc ccc aag tca gac tcc aaa gcc ctt gac ctg ctg gac Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp 545 550 560	1680
cgg atg tta acc ttt aac ccc aat aaa cgg atc aca gtg gag gaa gcg Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala 565 570 575	1728
ctg gct cac ccc tac ctg gag cag tac tat gac ccg acg gat gag cca Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro 580 585 590	1776
gtg gcc gag gag ccc ttc acc ttc gcc atg gag ctg gat gac cta cct Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro 595 600 605	1824
aag gag cgg ctg aag gag ctc atc ttc cag gag aca gca cgc ttc cag Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln 610 615 620	1872
ccc gga gtg ctg gag gcc ccc tag Pro Gly Val Leu Glu Ala Pro 625 630	1896
<210> 6 <211> 631 <212> PRT <213> Aequorea victoria and human	
<400> 6	
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 . 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 . 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala 245 250 255

Ala Ala Gln Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val 260 265 270

Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe 275 280 285

Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala 290 295 300

Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val 305 310 315 320

Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg 325 330 335

Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val 340 345 350

Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg 355 360 365

Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu 370 380

Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr 385 390 395 400

Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His 405 410 415

Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu 420 425 430

Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp 435 440 445

His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala 450 460

<400> 7

Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile 470 475 Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile 485 490 Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile 505 500 Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys 515 Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp 535 Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp 550 555 Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala 565 570 Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro 580 585 Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro 595 600 605 Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln 610 Pro Gly Val Leu Glu Ala Pro 625 <210> 7 <211> 2160 <212> DNA <213> Aequorea victoria and human <220> <221> CDS <222> (1)..(2160) <223>

							ccc Pro		4	18
							gtg Val 30		ğ	96
							aag Lys		14	14
							gtg Val		19	92
							cac His		24	4 Ö
							gtc Val		28	38
							cgc Arg 110		33	36
							ctg Leu		38	84
_	_	 _					ctg Leu		43	32
	-		_				cag Gln		4 8	80
							gac Asp		52	28
							ggc Gly 190		51	76
							tcc Ser		62	24
							ctg Leu		6	72

					atc Ile 230									720
		_		_	gct Ala		_	_		_		-		768
_			_	_	cca Pro	_	-	_	_	_				816
					gga Gly									864
					gag Glu									912
					tta Leu 310									960
					tgt Cys									1008
		_	_		cca Pro		_		_	_				1056
		_			gaa Glu						-	 -		1104
_			_		gga Gly	-			_					1152
-			_		cac His 390	-								1200
					aat Asn									1248
					gtt Val									1296
	_				atc Ile			-		_				1344

					-						gca Ala 460					1392
											gga Gly					1440
_		-		_	_		_	_			agt Ser	_	_			1488
		_	_								cct Pro					1536
											gca Ala				. •	1584
											gaa Glu 540					1632
											gac Asp					1680
											aac Asn					1728
-	_	_		_							gtg Val					1776
			_	_		_		-		-	gat Asp	-	-			1824
	_	_			_						tgg Trp 620					1872
	_						-		_	_	atc Ile			_		1920
											cag Gln					1968
											atg Met					2016

G] À āāā																2064	1
tgg Trp											tgg Trp 700					2112	2
tta Leu 705											tca Ser				taa	2160)
<210 <211 <212 <213	>	3 719 PRT Aequo	orea [.]	vict	coria	a and	d hur	nan									
<400)> {	3															
Met 1	Val	Ser	Lys	Gly 5	Glu	Glu	Leu	Phe	Thr 10	Gly	Val	Val	Pro	Ile 15	Leu	!	
Val	Glu	Leu	Asp 20	Gly	Asp	Val	Asn	Gly 25	His	Lys	Phe	Ser	Val 30	Ser	Gly		
Glu	Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile		
Cys	Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr		
Leu 65	Thr	Tyr	Gly	Val	Gln 70	Cys	Phe	Ser	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80		
Gln	His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu		
Arg	Thr	Ile	Phe 100	Phe	Lys	Asp	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu		
Val	Lys	Phe 115	Glu	Gly	Asp	Thr	Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly		
Ile	Asp 130	Phe	Lys	Glu	Asp	Gly 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr		

Asn 145	Tyr	Asn	Ser	His	Asn 150	Val	Tyr	Ile	Met	Ala 155	Asp	Lys	Gln	Lys	Asn 160
Gly	Ile	Lys	Val	Asn 165	Phe	Lys	Ile	Arg	His 170	Asn	Ile	Glu	Asp	Gly 175	Ser
Val	Gln	Leu	Ala 180	Asp	His	Tyr	Gln	Gln 185	Asn	Thr	Pro	Ile	Gly 190	Asp	Gly
Pro	Val	Leu 195	Leu	Pro	Asp	Asn	His 200	Tyr	Leu	Ser	Thr	Gln 205	Ser	Ala	Leu
Ser	Lys 210	Asp	Pro	Äsn	Glu	Lys 215	Arg	Asp	His	Met	Val 220	Leu	Leu	Glu	Phe
Val 225	Thr	Ala	Ala	Gly	Ile 230	Thr	Leu	Gly	Met	Asp 235	Glu	Leu	Tyr	Lys	Ser 240
Gly	Leu	Arg	Ser	Arg 245	Ala	Gln	Ala	Ser	Asn 250	Ser	Thr	Met	Ser	Ser 255	Ile
Leu	Pro	Phe	Thr 260	Pro	Pro	Val	Val	Lys 265	Arg	Leu	Leu	Gly	Trp 270	Lys	Lys
Ser	Ala	Gly 275	Gly	Ser	Gly	Gly	Ala 280	Gly	Gly	Gly	Glu	Gln 285	Asn	Gly	Gln
Glu	Glu 290	Lys	Trp	Cys	Glu	Lys 295	Ala	Val	Lys	Ser	Leu 300	Val	Lys	Lys	Leu
Lys 305	Lys	Thr	Gly	Arg	Leu 310	Asp	Glu	Leu	Glu	Lys 315	Ala	Ile	Thr	Thr	Gln 320
Asn	Cys	Asn	Thr	Lys 325	Cys	Val	Thr	Ile	Pro 330	Ser	Thr	Cys	Ser	Glu 335	Ile
Trp	Gly	Leu	Ser 340	Thr	Pro	Asn	Thr	Ile 345	Asp	Gln	Trp	Asp	Thr 350	Thr	Gly
Leu	Tyr	Ser 355	Phe	Ser	Glu	Gln	Thr 360	Arg	Ser	Leu	Asp	Gly 365	Arg	Leu	Gln

Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp 370 380

Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn 385 390 395 400

Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro 405 410 415

Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val
420 425 430

Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr \cdot 435 440 445

Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro 450 455 460

Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu 465 470 475 480

Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly 485 490 495

Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser 500 505 510

Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser 515 520 525

Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala 530 540

Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser 545 550 555 560

Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr 565 570 575

Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr \cdot 580 585 590

Ile	Gly	G1y 595	GIu	Val	Phe	Ala	600	Cys	Leu	Ser	Asp	Ser 605	Ala	IIe	Phe	
Val	Gln 610	Ser	Pro	Asn	Cys	Asn 615	Gln	Arg	Tyr	Gly	Trp 620	His	Pro	Ala	Thr	
Val 625	Cys	Lys	Ile	Pro	Pro 630	Gly	Cys	Asn	Leu	Lys 635	Ile	Phe	Asn	Asn	Gln 640	
Glu	Phe	Ala	Ala	Leu 645	Leu	Ala	Gln	Ser	Val 650	Asn	Gln	Gly	Phe	Glu 655	Ala	
Val	Tyr	Gln	Leu 660	Thr	Arg	Met	Cys	Thr 665	Ile	Arg	Met	Ser	Phe 670	Val	Lys	
Gly	Trp	Gly 675	Ala	Glu	Tyr	Arg	Arg 680	Gln	Thr	Val	Thr	Ser 685	Thr	Pro	Cys	
Trp	Ile 690	Glu	Leu	His	Leu	Asn 695	Gly	Pro	Leu	Gln	Trp 700	Leu	Asp	Lys	Val	
Leu 705	Thr	Gln	Met	Gly	Ser 710	Pro	Ser	Val	Arg	Cys 715	Ser	Ser	Met	Ser		
<210 <211 <212 <213	L> 2 2> [2157 DNA	orea	vict	coria	a and	d hur	man								
<220 <221 <222 <223	L> (2>	CDS (1)	. (215	57)												
	tcg	tcc						ccg Pro								48
								tct Ser 25								96
								tgt Cys								144

	_	_	_				_		-	gag Glu 60		_			192
				_				-	_	acc Thr			_		240
										acg Thr					288
_					_			_		acc Thr				-	336
										cca Pro					384
_	_		 _			-			_	cat His 140					432
_		_	_	_		-				aaa Lys	_	_	_	_	480
-	-					_	_	-		aca Thr		-			528
	-			_						aca Thr					576
	_	_						_		act Thr				_	624
			_	-					-	acg Thr 220					672
										cag Gln					720
										act Thr					768
										tac Tyr					816

	, ,	-			gca Ala			-			-		_		_	864
					cag Gln											912
					agg Arg 310		_							_		960
_		_	,	_	gaa Glu	_		_					_			1008
_					ggt Gly		-	-		_		_		_	_	1056
_	_				cag Gln	-			-		_	-				1104
		_			tgt Cys						_		_	_		1152
					ttt Phe 390											1200
		_	_	-	tat Tyr	_			_	_	_			-		1248
_					tgg Trp		_	_		_						1296
					att Ile											1344
_	-		-		act Thr	_	_						_	_		1392
_	_			-	ccg Pro 470		_		-		_	_	_		_	1440
					gag Glu											1488

 -	-		-	gta Val											1536
 		-	_	acc Thr			_	_		_	_			-	1584
				ccc Pro											1632
			_	tgc Cys 550		-	_								1680
				tcc Ser											1728
			_	gac Asp	_				-		_	_			1776
				acc Thr											1824
				ggc Gly											1872
				gtc Val 630											1920
_				aag Lys		_					-		_		1968
	_	_		tac Tyr	_	_						_			2016
 -	_			aac Asn											2064
-				aag Lys	-	-		_	-	-	-			-	2112
-	-			act Thr 710			-	-		_		_	taa		2157

```
<210> 10
<211> 718
<212> PRT
<213> Aequorea victoria and human
<400> 10
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
            ( 5
                                   10
Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Glu Glu
           20
Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
                    . 40
Val Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
                   70
                                       75
Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
                                   90
               85
Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
           100
                               105
                                                   110
Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
       115
                           120
Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
    130
                       135
Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
145
                   150
Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
```

165

180

190

170

Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro

185

Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala 195 200 205

Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly 210 215 220

Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser 225 230 235 240

Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro 245 250 255

Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala 260 265 270

Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu 275 280 285

Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp 290 295 300

Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn 305 310 315 320

Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val 325 330 335

Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp 340 345 350

Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp 355 360 365

His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile $370 \hspace{1cm} 375 \hspace{1cm} 380$

Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln 385 390 395 400

Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met 405 410 415

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430$

Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp 435 440 445

Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser 450 460

Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met 465 470 475 480

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 485 490 495

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 500 505 510

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 515 520 525

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 530 540

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln 545 550 555 560

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 565 570 575

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 580 585 590

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 595 600 605

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 610 615 620

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 625 630 635 640

	Val	Asn	Phe 645	Lys	Ile	Arg	His	Asn 650	Ile	Glu	Asp	Gly	Ser 655	Val	
Gln Leu		Asp 660	His	Tyr	Gln	Gln	Asn 665	Thr	Pro	Ile	Gly	Asp 670	Gly	Pro	
Val Leu	Leu 675	Pro	Asp	Asn	His	Tyr 680	Leu	Ser	Thr	Gln	Ser 685	Ala	Leu	Ser	
Lys Asp 690	Pro	Asn	Glu	Lys	Arg 695	Asp	His	Met	Val	Leu 700	Leu	Glu	Phe	Val	
Thr Ala 705	Ala	Gly	İle	Thr 710	Leu	Gly	Met	Asp	Glu 715	Leu	Tyr	Lys		·	
<211> 3 <212> 1	l1 l908 DNA Aequo	orea	vict	coria	a and	d hum	nan								
	CDS (1)	(190	08)												
<400> : atg gtg Met Val 1															48
atg gtg Met Val	agc Ser	Lys	Gly 5 ggc	Glu gac	Glu gta	Leu aac	Phe ggc	Thr 10 cac	Gly	Val ttc	Val agc	Pro gtg	Ile 15 tcc	Leu	48 96
atg gtg Met Val 1 gtc gag	agc Ser ctg Leu	Lys gac Asp 20	Gly 5 ggc Gly gat	Glu gac Asp	Glu gta Val acc	Leu aac Asn	ggc Gly 25	Thr 10 cac His	Gly aag Lys ctg	ttc Phe	Val agc Ser	Pro gtg Val 30	Ile 15 tcc Ser	ggc Gly	
atg gtg Met Val 1 gtc gag Val Glu gag ggc	agc Ser ctg Leu gag Glu 35	gac Asp 20 ggc Gly	Gly 5 ggc Gly gat Asp	Glu gac Asp gcc Ala	gta Val acc Thr	aac Asn tac Tyr 40	ggc Gly 25 ggc Gly	Thr 10 cac His aag Lys	aag Lys ctg Leu	ttc Phe acc Thr	agc Ser ctg Leu 45	gtg Val 30 aag Lys	tcc Ser ttc Phe	ggc Gly atc Ile	96
atg gtg Met Val 1 gtc gag Val Glu gag ggc Glu Gly tgc acc Cys Thr	agc Ser ctg Leu gag Glu 35 acc Thr	Lys gac Asp 20 ggc Gly ggc Gly	Gly 5 ggc Gly gat Asp aag Lys	gac Asp gcc Ala ctg Leu	gta Val acc Thr ccc Pro 55	Leu aac Asn tac Tyr 40 gtg Val	ggc Gly 25 ggc Gly ccc Pro	Thr 10 cac His aag Lys tgg Trp	aag Lys ctg Leu ccc Pro	ttc Phe acc Thr acc Thr 60	agc Ser ctg Leu 45 ctc Leu	gtg Val 30 aag Lys gtg Val	Ile 15 tcc Ser ttc Phe acc Thr	ggc Gly atc Ile acc Thr	96 144

				aag Lys										336
				gac Asp										384
				gac Asp										432
		_		aac Asn 150	-			_	_	_		_		480
				ttc Phe										528
 -		_	-	cac His		_	_						-	576
				gac Asp										624
				gag Glu										672
	-	_		atc Ile 230										720
	_		_	gct Ala		_		_	_		_	-		768
				tgt Cys										816
				tgg Trp										864
				tac Tyr										912
 		_	_	cag Gln 310		-	_	_		-				960

							aac Asn							10	80
	_	-	_	_	_	-	tgg Trp							10	56
_		_	_		_	-	ggc Gly 360	_	_	_	_		 _	11	04
_							ccc Pro							11	52
							gag Glu							12	00
							gag Glu							12	48
		_			-		ggt Gly							12	96
							ccc Pro 440							13	44
	-	_				-	ggg Gly							13	92
							ggt Gly							14	40
							gcc Ala							14	88
							aca Thr							15	36
							gaa Glu 520							15	84
							ggg Gly							16	32

Ala Asn Gln Glu Gl 545		cc aga gtc ccg la Arg Val Pro 555		
gtg cgg aga ccc tg Val Arg Arg Pro Ti 50				
tcg tct tct tcg gt Ser Ser Ser Ser Va 580				
tcc agt gat tac to Ser Ser Asp Tyr Se 595	er Asp Leu G			
gag gtg aag aag ga Glu Val Lys Lys Gl 610				
ttc gtc cag gag ct Phe Val Gln Glu Le 625				1908
<210> 12 <211> 635				
<212> PRT <213> Aequorea v	ictoria and b	human		
	ictoria and 1	human		
<213> Aequorea v			Val Val Pro	Ile Leu 15
<213> Aequorea vi <400> 12 Met Val Ser Lys G	ly Glu Glu Le	eu Phe Thr Gly 10		15
<213> Aequorea vi <400> 12 Met Val Ser Lys Gi 1 5	ly Glu Glu Le ly Asp Val A	eu Phe Thr Gly 10 sn Gly His Lys 25 yr Gly Lys Leu	Phe Ser Val	15 Ser Gly
<213> Aequorea vi <400> 12 Met Val Ser Lys Gi 1 5 Val Glu Leu Asp Gi 20 Glu Gly Glu Gly As	ly Glu Glu Le ly Asp Val As sp Ala Thr T	eu Phe Thr Gly 10 sn Gly His Lys 25 yr Gly Lys Leu 0	Phe Ser Val 30 Thr Leu Lys 45	Ser Gly Phe Ile
<213> Aequorea vi <400> 12 Met Val Ser Lys Gi 1 5 Val Glu Leu Asp Gi 20 Glu Gly Glu Gly As 35 Cys Thr Thr Gly Ly	ly Glu Glu Le ly Asp Val As sp Ala Thr Ty 40 ys Leu Pro Va 55	eu Phe Thr Gly 10 sn Gly His Lys 25 yr Gly Lys Leu 0	Phe Ser Val 30 Thr Leu Lys 45 Thr Leu Val 60	Ser Gly Phe Ile Thr Thr

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met $245 \\ \hspace{1.5cm} 250 \\ \hspace{1.5cm} 255$

Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp 260 265 270

Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe 275 280 285

Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val 290 295 300

Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala 305 310 315 320 Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln 325 330 335

Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu 340 345 350

Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu 355 360 365

Glu Gly Gly Gly Pro Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val 370 375 380

Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln 385 390 395 400

Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly $405 \hspace{1cm} 410 \hspace{1cm} 415$

Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro 420 425 430

Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val435 440 445

Pro Ala Ala Ala His Gly Ala Gly Gly Pro Pro Pro Ala Pro Pro 450 455 460

Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Ala Gly Ala Pro Gly 465 470 475 480

Leu Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln 485 490 495

Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg 500 505 510

Ser Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg 515 520 525

Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser 530 540

Ala Asn Gln Glu 545	Glu Pro G 550	Glu Ala Arg	Val Pro 555	Ala Gln	Ser Glu	Ser 560
Val Arg Arg Pro	Trp Glu I 565	Lys Asn Ser	Thr Thr 570	Leu Pro	Arg Met 575	Lys
Ser Ser Ser Ser 580	Val Thr T	Thr Ser Glu 585		Pro Cys	Thr Pro 590	Ser
Ser Ser Asp Tyr 595	Ser Asp I	Leu Gln Arg 600	Val Lys	Gln Glu 605	Leu Leu	Glu
Glu Val Lys Lys 610		Gln Lys Val 515	Lys Glu	Glu Ile 620	Ile Glu	Ala
Phe Val Gln Glu 625	Leu Arg I 630	Lys Arg Gly	Ser Pro 635			
<210> 13 <211> 2394 <212> DNA <213> Aequorea	victoria	and human				
<220> <221> CDS <222> (1)(23 <223>	94)					
<400> 13 atg gtg agc aag Met Val Ser Lys 1						
gtc gag ctg gac Val Glu Leu Asp 20						
gag ggc gag ggc Glu Gly Glu Gly 35						
tgc acc acc ggc Cys Thr Thr Gly 50	Lys Leu B					

							atg Met							288
_				_	-	_	ggc Gly 105			_				336
							gtg Val							384
	_	_		-			atc Ile	_			_	_		432
		_			-		atc Ile	_	_	-		-		480
							cgc Arg							528
	_	_	_			_	cag Gln 185							576
							tac Tyr							624
							gat Asp							672
							ggc Gly							720
							gaa Glu							768
							ccc Pro 265							816
							cgc Arg							864
							agc Ser							912

	atc Ile							960
	gtc Val							1008
	aag Lys							1056
	tgc Cys 355							1104
	gac Asp							1152
	ttc Phe							1200
	gtg Val							1248
	ctc Leu							1296
	ccc Pro 435							1344
	agc Ser							1392
	aaa Lys							1440
	ggc Gly							1488
	cgg Arg							1536
	tcc Ser 515							1584

	_	-		_		-		-		_	gat Asp 540	_				1632
			_								aag Lys	_		_	-	1680
-	_			-				_			cct Pro					1728
	_				-	-					ccc Pro					1776
											atc Ile					1824
											agc Ser 620					1872
											gct Ala					1920
	_		_	_	-		_	_	-	-	gcc Ala		_		-	1968
	_		-					_	_		gcc Ala			-		2016
											gag Glu					2064
											ctt Leu 700					2112
											gac Asp					2160
_	_	_	_		_					-	ccc Pro					2208
	_	_	_								cgc Arg					2256

-	_				-		-		_		ctg Leu				ggg Gly	2	304
								-	-	-	ttc Phe 780					2	352
-	_	-			_	_	_	_	_		agc Ser		taa			2	394
<210 <211 <211 <211	1>	14 797 PRT Aequo	orea	vict	coria	a and	d hur	man									
<400	0> :	14															
Met 1	Val	Ser	Lys	Gly 5	Glu	Glu	Leu	Phe	Thr 10	Gly	Val	Val	Pro	Ile 15	Leu		
Val	Glu	Leu	Asp 20	Gly	Asp	Val	Asn	Gly 25	His	Lys	Phe	Ser	Val 30	Ser	Gly		
Glu	Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile		
Cys	Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr		
Leu 65	Thr	Tyr	Gly	Val	Gln 70	Cys	Phe	Ser	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80		
Gln	His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu		
Arg	Thr	Ile	Phe 100	Phe	Lys	Asp	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu		
Val	Lys	Phe 115	Glu	Gly	Asp	Thr	Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly		
Ile	Asp 130	Phe	Lys	Glu	Asp	Gly 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr		

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 150 155 145 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 170 165 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 200 . 195 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 215 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 230 235 Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro 245 250 Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln 260 265 Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser 280 275 Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His 295 290 Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile 315 310

Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro 340 345 350

Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu

330

Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys 355 360 365

Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn 370 380

Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu 385 390 395 400

Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly 405 410 415

Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn 420 425 430

Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn 435 440 445

Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys 450 455 460

Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu 465 470 475 480

Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile 485 490 495

Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val 500 505 510

Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu 515 520 525

Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile 530 540

Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys 545 550 555 560

Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg 565 570 575

Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro 580 585 590

Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu
595 600 605

Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala 610 615 620

Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala 625 630 635 640

Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val 645 650 655

Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro 660 665 670

Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln 675 680 685

Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr 690 695 700

Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu
725 730 735

Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly
740 745 750

Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly 755 760 765

Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala 770 780

Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser 785 790 795

<210> 15

<211> 2394

<212> DNA

<213> Aequorea victoria and human

<2 <2	220 221 222 223	> (CDS (1)	(239	94)			·					
at	g		gaa				atc Ile						48
							att Ile						96
							ggg Gly 40						144
							aag Lys						192
	Ĺу						gtg Val						240
							cac His						288
							ctc Leu						336
							tgt Cys 120						384
	La						acc Thr						432
	Le						tac Tyr						480
							cca Pro						528
							ttt Phe						576

				cga Arg										624
 -				cta Leu	_	_	-	-						672
				gga Gly 230										720
				cga Arg										768
				ctg Leu										816
				cgg Arg										864
				gat Asp										912
				aag Lys 310										960
	-			cct Pro			-	-						1008
				ccc Pro										1056
				atc Ile										1104
		_		agc Ser	_	-	_	_	_	_				1152
_	_		_	gct Ala 390		_		_		_	-	-	-	1200
_	_	_	_	gcc Ala										1248

					gcc Ala										1296
_		_	_		gag Glu	-	_	_	_	_	_		-		1344
					ctt Leu										1392
-	_	-		-	gac Asp 470					_	_	_	-		1440
				_	ccc Pro						_	_	_		1488
					cgc Arg										1536
					ctg Leu										1584
		_	_	_	ttc Phe						-	-			1632
-	_	-	-		agc Ser 550										1680
-	-				ctg Leu								-	_	 1728
-	_		-	_	aac Asn			_		_					 1776
		_			tac Tyr		_	_		_	_			-	1824
					gtg Val										1872
			_	-	ttc Phe 630	-	-			_		-	_	-	1920

Asp Phe Phe Lys		aa ggc tac gtc cag g u Gly Tyr Val Gln C 650	
_	Asp Asp Gly Asn T	ac aag acc cgc gcc ovr Lys Thr Arg Ala (
		gc atc gag ctg aag o cg Ile Glu Leu Lys (685	
		gg cac aag ctg gag t Ly His Lys Leu Glu 1 700	
		cc gac aag cag aag a la Asp Lys Gln Lys A 715	
Lys Val Asn Phe		ac atc gag gac ggc a sn Ile Glu Asp Gly S 730	
	Tyr Gln Gln Asn T	cc ccc atc ggc gac o nr Pro Ile Gly Asp (15	
		gc acc cag tcc gcc o er Thr Gln Ser Ala 1 765	
		ng gtc ctg ctg gag f et Val Leu Leu Glu 1 780	
		ac gag ctg tac aag s sp Glu Leu Tyr Lys 795	taa 2394
•	victoria and huma	ח	
_	Phe Pro Leu Ile P 5	ne Pro Ala Glu Pro <i>i</i> 10	Ala Gln Ala 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met 20 25 30

Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly 35 40 45

Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn 50 55 60

Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp 65 70 75 80

Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg 85 90 95

Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser 100 105 110

Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln 115 120 125

Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro 130 135 140

Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys 145 150 155 160

Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro 165 170 175

Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala 180 185 190

Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205

Gly Asp Glu Ile Phe Leu Cys Asp Lys Val Gln Lys Glu Asp Ile 210 215 220

Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser 225 230 235 240

Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro 245 250 255

Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu 260 265 Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr 275 280 285 Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Lys Arg Lys Arg 290 295 Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly 305 315 310 320 Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg 325 330 Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr 345 Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe 355 360 365 Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro 375 Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val 385 390 395 400 Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly 405 410 415 Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly 420 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu 435 440 445

Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr 450 455 460

Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln 465 470 475 480

Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr 485 490 495

Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp 500 505 510

Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu 515 520 525

Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala 530 540

Leu Leu Ser Gln Ile Ser Ser Leu Asp Pro Pro Val Ala Thr Met Val 545 550 555 560

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 565 570 575

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 580 585 590

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 595 600 605

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr 610 615 620

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 625 630 635 640

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 645 650 655

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys $660 \hspace{1.5cm} 665 \hspace{1.5cm} 670$

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp 675 680 685

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr 690 695 700

705	Val Tyr 710	Ile Met	Ala Asp	Lys Gln 715	Lys Asn	Gly Ile 720	
Lys Val Asn Phe	Lys Ile 725	Arg His	Asn Ile 730	Glu Asp	Gly Ser	Val Gln 735	
Leu Ala Asp His 740	_		Thr Pro 745	Ile Gly	Asp Gly 750	Pro Val	
Leu Leu Pro Asp 755	Asn His	Tyr Leu 760	Ser Thr	Gln Ser	Ala Leu 765	Ser Lys	
Asp Pro Asn Glu 770	Lys Arg	Asp His 775	Met Val	Leu Leu 780	Glu Phe	Val Thr	. `
Ala Ala Gly Ile 785	Thr Leu 790	Gly Met	Asp Glu	Leu Tyr 795	Lys		
<210> 17 <211> 2757 <212> DNA <213> Aequorea	victoria	a and hum	nan				
<220> <221> CDS							
<222> (1)(2° <223>	'57) '						
<222> (1)(2	ı ggc gag						48
<222> (1)(27 <223> <400> 17 atg gtg agc aag Met Val Ser Lys	g ggc gag s Gly Glu 5 s ggc gac	Glu Leu gta aac	Phe Thr 10 ggc cac	Gly Val	Val Pro	Ile Leu 15 tcc ggc	48 96
<222> (1)(2° <223> <400> 17 atg gtg agc aag Met Val Ser Lys 1 gtc gag ctg gag Val Glu Leu Asp	g ggc gag Gly Glu 5 ggc gac Gly Asp	Glu Leu gta aac Val Asn	Phe Thr 10 ggc cac Gly His 25 ggc aag	Gly Val aag ttc Lys Phe ctg acc	Val Pro agc gtg Ser Val 30 ctg aag	<pre>Ile Leu 15 tcc ggc Ser Gly ttc atc</pre>	
<222> (1)(27 223 <400> 17 atg gtg agc aag Met Val Ser Lys 1 gtc gag ctg gag Val Glu Leu Asp 20 gag ggc gag ggg Glu Gly Glu Gly	g ggc gag Gly Glu 5 ggc gac Gly Asp gat gcc Asp Ala	Glu Leu gta aac Val Asn acc tac Thr Tyr 40 ccc gtg	Phe Thr 10 ggc cac Gly His 25 ggc aag Gly Lys ccc tgg	Gly Val aag ttc Lys Phe ctg acc Leu Thr ccc acc	Val Pro agc gtg Ser Val 30 ctg aag Leu Lys 45 ctc gtg	<pre>Ile Leu 15 tcc ggc Ser Gly ttc atc Phe Ile acc acc</pre>	96

					aag Lys										288
	_				aag Lys	-	-			_		_	-		336
		_			 gac Asp		_		-			-			384
		-		_	 gac Asp			_			_	_			432
				_	aac Asn 150	-		_	-	-	-	_			480
					ttc Phe										528
					cac His										576
•					gac Asp										624
	_		-		gag Glu	_	_								672
					atc Ile 230										720
					ggc Gly										768
					gag Glu										816
					gtg Val										864
					ccc Pro										912

tgg Trp 305	ggc Gly	ttc Phe	ggg Gly	aag Lys	cag Gln 310	gga Gly	ttc Phe	cag Gln	tgc Cys	caa Gln 315	gtt Val	tgc Cys	tgc Cys	ttt Phe	gtg Val 320	960
											tcc Ser					1008
											aaa Lys					1056
											cac His					1104
											gac Asp 380					1152
											agc Ser					1200
											cag Gln					1248
											aaa Lys					1296
											aaa Lys					1344
											aaa Lys 460					1392
											ttt Phe					1440
											tgg Trp					1488
											ttt Phe					1536
											tta Leu					1584

		aat Asn									1632
		cag Gln 550									1680
		gaa Glu								٠	1728
		gac Asp									1776
		ggc Gly									1824
		ctc Leu									1872
		gac Asp 630									1920
		aag Lys									1968
		cgc Arg									2016
		cac His									2064
		gct Ala									2112
		att Ile 710									2160
_		 cac His	_	-	-		_	_	_		2208
		ggg Gly									2256

-		tat cag ccc tat ggg Tyr Gln Pro Tyr Gly 765	-
		ctg tat gaa atg ttg Leu Tyr Glu Met Leu 780	
		gat gaa ctc ttc caa Asp Glu Leu Phe Gln 795	
	, ,	tct atg tcc aag gaa Ser Met Ser Lys Glu 810	, , ,
= =		cac cca ggc aaa cgt His Pro Gly Lys Arg 830	
		aaa gag cat gca ttt Lys Glu His Ala Phe 845	= =
		aaa gag atc cag ccc Lys Glu Ile Gln Pro 860	
= = = = = = = = = = = = = = = = = = = =		acc tcc aac ttc gac Thr Ser Asn Phe Asp 875	
		ccc act gat aaa ctc Pro Thr Asp Lys Leu 890	
	Gln Asn Glu Phe Ala	ggc ttc tct tat act Gly Phe Ser Tyr Thr 910	
gag ttt gtc att Glu Phe Val Ile 915			2757
<210> 18 <211> 918 <212> PRT <213> Aequorea	victoria and human		
<400> 18			
Met Val Ser Lys 1	Gly Glu Glu Leu Pho 5	Thr Gly Val Val Pro	Ile Leu 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240

Gly Leu Arg Ser Arg Gly Lys Met Ala Asp Pro Ala Ala Gly Pro Pro 245 250 255

Pro Ser Glu Glu Glu Ser Thr Val Arg Phe Ala Arg Lys Gly Ala 260 265 270

Leu Arg Gln Lys Asn Val His Glu Val Lys Asn His Lys Phe Thr Ala 275 280 285

Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr Asp Phe Ile 290 295 300

Trp Gly Phe Gly Lys Gln Gly Phe Gln Cys Gln Val Cys Cys Phe Val 305 310 315 320

Val His Lys Arg Cys His Glu Phe Val Thr Phe Ser Cys Pro Gly Ala 325 330 335

Asp Lys Gly Pro Ala Ser Asp Asp Pro Arg Ser Lys His Lys Phe Lys 340 345 350

Ile His Thr Tyr Ser Ser Pro Thr Phe Cys Asp His Cys Gly Ser Leu 355 360 365

Leu Tyr Gly Leu Ile His Gln Gly Met Lys Cys Asp Thr Cys Met Met 370 380

Asn Val His Lys Arg Cys Val Met Asn Val Pro Ser Leu Cys Gly Thr 385 390 395 400

Asp His Thr Glu Arg Arg Gly Arg Ile Tyr Ile Gln Ala His Ile Asp 405 410 415

Arg Asp Val Leu Ile Val Leu Val Arg Asp Ala Lys Asn Leu Val Pro $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430$

Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys Leu Lys Leu Ile 435 440 445

Pro Asp Pro Lys Ser Glu Ser Lys Gln Lys Thr Lys Thr Ile Lys Cys 450 455 460

Ser Leu Asn Pro Glu Trp Asn Glu Thr Phe Arg Phe Gln Leu Lys Glu 465 470 475 480

Ser Asp Lys Asp Arg Arg Leu Ser Val Glu Ile Trp Asp Trp Asp Leu 485 490 495

Thr Ser Arg Asn Asp Phe Met Gly Ser Leu Ser Phe Gly Ile Ser Glu 500 505 510

Leu Gln Lys Ala Ser Val Asp Gly Trp Phe Lys Leu Leu Ser Gln Glu 515 520 525

Glu Gly Glu Tyr Phe Asn Val Pro Val Pro Pro Glu Gly Ser Glu Ala 530 535 540

Asn Glu Glu Leu Arg Gln Lys Phe Glu Arg Ala Lys Ile Ser Gln Gly 545 550 555 560

Thr Lys Val Pro Glu Glu Lys Thr Thr Asn Thr Val Ser Lys Phe Asp 565 570 575

Asn Asn Gly Asn Arg Asp Arg Met Lys Leu Thr Asp Phe Asn Phe Leu 580 585 590

Met Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ser Glu Arg 595 600 605

Lys Gly Thr Asp Glu Leu Tyr Ala Val Lys Ile Leu Lys Lys Asp Val 610 620

Val Ile Gln Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val 625 630 635 640

Leu Ala Leu Pro Gly Lys Pro Pro Phe Leu Thr Gln Leu His Ser Cys 645 650 655

Phe Gln Thr Met Asp Arg Leu Tyr Phe Val Met Glu Tyr Val Asn Gly 660 665 670

Gly Asp Leu Met Tyr His Ile Gln Gln Val Gly Arg Phe Lys Glu Pro 675 680 685 His Ala Val Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe Phe Leu 690 695 700

Gln Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Met 705 710 715 720

Leu Asp Ser Glu Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys 725 730 735

Glu Asn Ile Trp Asp Gly Val Thr Thr Lys Thr Phe Cys Gly Thr Pro
740 745 750

Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr Gln Pro Tyr Gly Lys Ser 755 760 765

Val Asp Trp Trp Ala Phe Gly Val Leu Leu Tyr Glu Met Leu Ala Gly 770 775 780

Gln Ala Pro Phe Glu Gly Glu Asp Glu Asp Glu Leu Phe Gln Ser Ile 785 790 795 800

Met Glu His Asn Val Ala Tyr Pro Lys Ser Met Ser Lys Glu Ala Val 805 810 815

Ala Ile Cys Lys Gly Leu Met Thr Lys His Pro Gly Lys Arg Leu Gly 820 825 830

Cys Gly Pro Glu Gly Glu Arg Asp Ile Lys Glu His Ala Phe Phe Arg 835 840 845

Tyr Ile Asp Trp Glu Lys Leu Glu Arg Lys Glu Ile Gln Pro Pro Tyr 850 855 860

Lys Pro Lys Ala Arg Asp Lys Arg Asp Thr Ser Asn Phe Asp Lys Glu 865 870 875

Phe Thr Arg Gln Pro Val Glu Leu Thr Pro Thr Asp Lys Leu Phe Ile 885 890 895

Met Asn Leu Asp Gln Asn Glu Phe Ala Gly Phe Ser Tyr Thr Asn Pro $900 \hspace{1.5cm} 905 \hspace{1.5cm} 910$

Glu Phe Val Ile Asn Val

```
915
<210> 19
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer used to construct the PKAc-F64L-S65T-GFP fusion
<400> 19
ttggacacaa gctttggaca ccctcaggat atgggcaacg ccgccgccgc caag
                                                                     54
<210> 20
<211> 55
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer used to construct the PKAc-F64L-S65T-GFP fusion
<400> 20
                                                                     55
qtcatcttct cgaqtctttc aggcgcgccc aaactcagta aactccttgc cacac
<210> 21
<211> 53
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer used to construct the PKAc-F64L-S65T-GFP fusion
ttggacacaa gctttggaca cggcgcgcca tgagtaaagg agaagaactt ttc
                                                                     53
<210> 22
<211> 53
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer used to construct the PKAc-F64L-S65T-GFP fusion
<400> 22
                                                                     53
gtcatcttct cgagtcttac tcctgaggtt tgtatagttc atccatgcca tgt
<210> 23
<211>
      55
<212> DNA
<213> Artificial sequence
```

	<220> <223>	Primer used to construct the PKC-GFP fusion	
	<400>	23	
	ttggac	acaa gctttggaca ccctcaggat atggctgacg tttacccggc caacg	55
	<210>	24	
		55	
		DNA	
	<213>	Artificial Sequence	
	<220>		
	<223>	Primer used to construct the PKC-GFP fusion	
	<400>	24	
	gtcatc	ttct cgagtctttc aggcgcgccc tactgcactt tgcaagattg ggtgc	55
	<210>	25	
		53	
₫		DNA	
Ţ		Artificial Sequence	
1		•	
اية : -	<220>		
	<223>	Primer used to construct the PKC-GFP fusion	
Ħ	<400>	25	
:F I 	ttggac	acaa gctttggaca cggcgcgcca tgagtaaagg agaagaactt ttc	53
	<210>	26	
<u>.1</u>		53	
ij		DNA	
<u> </u>	<213>	Artificial Sequence	
:eb	1000		
	<220> <223>	Primer used to construct the PKC-GFP fusion	
	\ 2237	Filmer used to constitute the FRC-GFF Tusion	
	<400>	26 .	
	gtcatc	ttct cgagtcttac tcctgaggtt tgtatagttc atccatgcca tgt	53
	<210>	27	
	<211>	30	
		DNA	
	<213>	Artificial Sequence	
	<220>	•	
		Primer targeted to Homo sapiens	
	<400>	27	
		tcaa ccatggcggc ggcggcggcg	30

	<210>	28	
	<211>	29	
	<212>	DNA	
	<213>	Artificial Sequence	
	<220>		
	<223>	Primer targeted to Homo sapiens	
	<400>	28	
		ccct agggggcctc cagcactcc	29
	· y y - · -		
	<210>	29·	
	<211>		
	<212>		
	<213>		
	<220>		
		Primer targeted to Homo sapiens	
	<400>	29	
<u></u>		tega ceatgtegte catettgeea tte	33
] A	9-9		
	<210>	30	
d	<211>		
Ú	<212>		
=======================================	<213>	Artificial Sequence	
n	.000		
	<220>	Dulman banashad ba Nama aasiana	
	<223>	Primer targeted to Homo sapiens	
	<400>	30	
≐ H	gtggta	cctt atgacatgct tgagcaacgc ac	32
	•		
.	<210>	31	
	<211>	33	
	<212>	DNA	
	<213>	Artificial Sequence	
	<220>		
	<223>	Primer targeted to Homo sapiens	
	<400>	31	
	gtgaat	toga coatgtogto catottgoca tto	33
	3 3		
	<210>	32	
	<211>		
	<212>		
		Artificial Sequence	
	<220>		
		Primer targeted to Homo saniens	

<400> 32

<213> Artificial Sequence

gtggtac	cca tgacatgctt gagcaacgca c	31
<210>	33	
<211>	29	
	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Primer targeted to Homo sapiens	
<400>	33	
gggaag	ette catgagegag aeggteate	29
<210>	34	
<211>	28	
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Primer targeted to Homo sapiens	
<400>	34	
cccggat	cet cagggagaac ecegette	28
<210>	35	
<211>	34	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Primer targeted to Homo sapiens	
<400>	35	
gtctcga	agec atggaegaae tgtteeeet eate	34
<210>	36	
<211>	32	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Primer targeted to Homo sapiens	
<400>	36	
gtggato	ectt aggagetgat etgaeteage ag	32
<210>	37	
<211>	34 .	
<212>	DNA	

	<220>		
	<223>	Primer targeted to Homo sapiens	
	<400>	37	٠.
	gtctcg	agcc atggacgaac tgttccccct catc	34
	•		
	<210>	38	
	<211>	31	
	<212>	DNA	
	<213>	Artificial Sequence	
	<220>		
	<223>	Primer targeted to Homo sapiens	
	\2237	Filmer Cargeted to homo sapiens	
	<400>	38	
	gtggat	ccaa ggagctgatc tgactcagca g	31
	<210>	39	
2	<211>	24	
	<212>	DNA	
ij	<213>	Artificial Sequence	
``~	<220>		
ᄖ	<223>	Primer targeted to Homo sapiens	
	<400>	39	
		ragge aagatggetg acce	24
 -	, ,		
::FI 1	<210>	40	
: :: 8	<211>	33	
i Li a.	<212>	DNA	
	<213>	Artificial Sequence	
1 = 11	<220>	·	
	<223>	Primer targeted to Homo sapiens	
	<400>	40	
	gtggat	ccct acacattaat gacaaactct ggg	33